

Thu Aug 1 12:01:46 2002

us-09-575-061-1.oligo.ram

Gabel
09/575061
Seq. ID 1 w/ Interf
Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 1, 2002, 10:51:17 ; Search time 109.3 Seconds
(without alignments)
1181.856 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 367
Sequence: 1 MRSKVALLIPALLAAGAAH.....TRDAGINTDVALGLVYQF 367

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 3502263 seqs, 351980561 residues

Word size : 50

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Pending Patents_AA_Main:*

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3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
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20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
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25: /cgn2_6/ptodata/2/paa/US101_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US102_COMB.pep.*

Pred. No. is the number of results predicted by the chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367	100.0	367	1	PCT-US01-16032A-1
2	367	100.0	367	1	PCT-US01-16032A-1
3	367	100.0	367	19	US-09-575-061-1
4	218	59.4	367	1	PCT-US99-05492-30
5	218	59.4	367	18	US-09-417-264-30
6	218	59.4	367	18	US-09-432-494-30
7	218	59.4	367	20	US-09-646-925-4

8	157	42.8	328	1	PCT-US01-08631-55900	Sequence 55900, A
9	157	42.8	759	1	PCT-US01-08631-56227	Sequence 56227, A
10	157	42.8	759	1	PCT-US01-08631-60152	Sequence 60152, A
11	127	34.6	393	1	PCT-US01-08631-55901	Sequence 55901, A
12	79	21.5	501	1	PCT-US01-08631-56224	Sequence 56224, A

ALIGNMENTS

RESULT 1
PCT-US01-16032A-1
Sequence 1, Application PC/TUS0116032
GENERAL INFORMATION:
APPLICANT: Cedars-Sinai Medical Center
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Crohn's Disease Using The Ompc Antigen
FILE REFERENCE: PP-PM 4713
CURRENT APPLICATION NUMBER: PCT/US01/16032
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 09/575,061
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 367
TYPE: PRT
ORGANISM: E. Coli
PCT-US01-16032A-1

Query Match 100.0%; Score 367; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSKVALLIPALLAAGAAHAAEVYNNKDKLIDYGVDSLHYFSNKKVDGQTYMRLG 60
DB 1 MRSKVALLIPALLAAGAAHAAEVYNNKDKLIDYGVDSLHYFSNKKVDGQTYMRLG 60
QY 61 FKGETVTDLTGTYGMEVQIQGNSAENENNSWTRVAFAGLKFQDVGSPFYGRNYGVYD 120
DB 61 FKGETVTDLTGTYGMEVQIQGNSAENENNSWTRVAFAGLKFQDVGSPFYGRNYGVYD 120
QY 121 VTSWTVLPEFGDITGSGDNFQKRGNFATYNTDFGLVDLNTAVYQGNKNGPSGE 180
DB 121 VTSWTVLPEFGDITGSGDNFQKRGNFATYNTDFGLVDLNTAVYQGNKNGPSGE 180
QY 181 GFISGVYNNRGRDALRONGDVGSGITTYDEFGIGAISSSKRTDAONTAAYTGNCDRAE 240
DB 181 GFISGVYNNRGRDALRONGDVGSGITTYDEFGIGAISSSKRTDAONTAAYTGNCDRAE 240
QY 241 TYTGGLKYDANNIYLAQYTYQYNAFVGSGLGMANKAQNFEAVAYOFDEGLRPSLAYIQ 300
DB 241 TYTGGLKYDANNIYLAQYTYQYNAFVGSGLGMANKAQNFEAVAYOFDEGLRPSLAYIQ 300
QY 301 SKKRNIGRGVDDDDILKYVDVGYATYFNKMASTYVYKILDLDDNOFTTRAGINTNTIYA 360
DB 301 SKKRNIGRGVDDDDILKYVDVGYATYFNKMASTYVYKILDLDDNOFTTRAGINTNTIYA 360
QY 361 LGLVYQF 367
DB 361 LGLVYQF 367

RESULT 2
PCT-US01-16032A-1
Sequence 1, Application PC/TUS0116032A
GENERAL INFORMATION:
APPLICANT: Targan, Stephan R.
APPLICANT: Braun, Jonathan
APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of

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; TITLE OF INVENTION: Crohn's Disease Using The OmpC Antigen
; FILE REFERENCE: FP-PW 4713
; CURRENT APPLICATION NUMBER: PCT/US01/16032A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 09/575,061
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 367
; TYPE: PRT
; ORGANISM: E. COLI
PCT-US01-16032A-1
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Query Match          100.0%; Score 367; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRSKVALLIIPALLAAGAAHAAEVYKDKGKLDLYGKVDGLHYFSDNKKVDGDDQTYMRIG 60
   1 MRSKVALLIIPALLAAGAAHAAEVYKDKGKLDLYGKVDGLHYFSDNKKVDGDDQTYMRIG 60
DB 1 MRSKVALLIIPALLAAGAAHAAEVYKDKGKLDLYGKVDGLHYFSDNKKVDGDDQTYMRIG 60
QY 61 FKGETVDTQLGYGQWQEQIOGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNGVYVD 120
   61 FKGETVDTQLGYGQWQEQIOGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNGVYVD 120
DB 61 FKGETVDTQLGYGQWQEQIOGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNGVYVD 120
QY 121 VTSMTDVLPEFGDPTGSDNFMQQRGNFGATYRNTDFGLVJGLNFAVQYQKNGNPSGE 180
   121 VTSMTDVLPEFGDPTGSDNFMQQRGNFGATYRNTDFGLVJGLNFAVQYQKNGNPSGE 180
DB 121 VTSMTDVLPEFGDPTGSDNFMQQRGNFGATYRNTDFGLVJGLNFAVQYQKNGNPSGE 180
QY 181 GFTSGVTNNGRDLRONGCVGSGSTYYDEGFGIGAISSSKRTDAQNTAAIYGNDRAE 240
   181 GFTSGVTNNGRDLRONGCVGSGSTYYDEGFGIGAISSSKRTDAQNTAAIYGNDRAE 240
DB 181 GFTSGVTNNGRDLRONGCVGSGSTYYDEGFGIGAISSSKRTDAQNTAAIYGNDRAE 240
QY 241 TYTGGLKYDANNITYLAAQYOTYTNATRVGSLGMANKAQNFEAVAOYQDFGLRPSLAYIQ 300
   241 TYTGGLKYDANNITYLAAQYOTYTNATRVGSLGMANKAQNFEAVAOYQDFGLRPSLAYIQ 300
DB 241 TYTGGLKYDANNITYLAAQYOTYTNATRVGSLGMANKAQNFEAVAOYQDFGLRPSLAYIQ 300
QY 301 SKGNLGRGYDDEDILKYVDGATYYFNKNMSTYYDYKINLLDNOFTRDAGINTDNIYA 360
   301 SKGNLGRGYDDEDILKYVDGATYYFNKNMSTYYDYKINLLDNOFTRDAGINTDNIYA 360
DB 301 SKGNLGRGYDDEDILKYVDGATYYFNKNMSTYYDYKINLLDNOFTRDAGINTDNIYA 360
QY 361 LGLVYQF 367
   361 LGLVYQF 367
DB 361 LGLVYQF 367
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RESULT 3
US-09-575-061-1
; Sequence 1, Application US/09575061
; GENERAL INFORMATION:
; APPLICANT: Targan, Stephan R.
; APPLICANT: Braun, Jonathan
; APPLICANT: Sutton, Christopher L.
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; FILE REFERENCE: P-PW 4097
; CURRENT APPLICATION NUMBER: US/09/575,061
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 367
; TYPE: PRT
; ORGANISM: E. COLI
US-09-575-061-1
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Query Match          100.0%; Score 367; DB 19; Length 367;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 367; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRSKVALLIIPALLAAGAAHAAEVYKDKGKLDLYGKVDGLHYFSDNKKVDGDDQTYMRIG 60
   1 MRSKVALLIIPALLAAGAAHAAEVYKDKGKLDLYGKVDGLHYFSDNKKVDGDDQTYMRIG 60
DB 1 MRSKVALLIIPALLAAGAAHAAEVYKDKGKLDLYGKVDGLHYFSDNKKVDGDDQTYMRIG 60
QY 61 FKGETVDTQLGYGQWQEQIOGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNGVYVD 120
   61 FKGETVDTQLGYGQWQEQIOGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNGVYVD 120
DB 61 FKGETVDTQLGYGQWQEQIOGNSAENENNSWTRVAFAGLKFQDVGSPDYGRNGVYVD 120
QY 121 VTSMTDVLPEFGDPTGSDNFMQQRGNFGATYRNTDFGLVJGLNFAVQYQKNGNPSGE 180
   121 VTSMTDVLPEFGDPTGSDNFMQQRGNFGATYRNTDFGLVJGLNFAVQYQKNGNPSGE 180
DB 121 VTSMTDVLPEFGDPTGSDNFMQQRGNFGATYRNTDFGLVJGLNFAVQYQKNGNPSGE 180
QY 181 GFTSGVTNNGRDLRONGCVGSGSTYYDEGFGIGAISSSKRTDAQNTAAIYGNDRAE 240
   181 GFTSGVTNNGRDLRONGCVGSGSTYYDEGFGIGAISSSKRTDAQNTAAIYGNDRAE 240
DB 181 GFTSGVTNNGRDLRONGCVGSGSTYYDEGFGIGAISSSKRTDAQNTAAIYGNDRAE 240
QY 241 TYTGGLKYDANNITYLAAQYOTYTNATRVGSLGMANKAQNFEAVAOYQDFGLRPSLAYIQ 300
   241 TYTGGLKYDANNITYLAAQYOTYTNATRVGSLGMANKAQNFEAVAOYQDFGLRPSLAYIQ 300
DB 241 TYTGGLKYDANNITYLAAQYOTYTNATRVGSLGMANKAQNFEAVAOYQDFGLRPSLAYIQ 300
QY 301 SKGNLGRGYDDEDILKYVDGATYYFNKNMSTYYDYKINLLDNOFTRDAGINTDNIYA 360
   301 SKGNLGRGYDDEDILKYVDGATYYFNKNMSTYYDYKINLLDNOFTRDAGINTDNIYA 360
DB 301 SKGNLGRGYDDEDILKYVDGATYYFNKNMSTYYDYKINLLDNOFTRDAGINTDNIYA 360
QY 361 LGLVYQF 367
   361 LGLVYQF 367
DB 361 LGLVYQF 367
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RESULT 4
PCT-US99-05492-30
; Sequence 30, Application PC/TUS9905492A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative
; FILE REFERENCE: UC PANCA Antigens
; TITLE OF INVENTION: Crohn's Disease Using The OmpC Antigen
; CURRENT APPLICATION NUMBER: PCT/US99/05492A
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 09/041,889
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 08/837,058
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Escherichia coli
PCT-US99-05492-30
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```

Query Match          59.4%; Score 218; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 2,1e-210;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 150 ATYRNTDFGLVDGLNFAVQYQKNGNPSGEGFTSGVTNNGRDLRONGDVGSGSTYYDY 209
   150 ATYRNTDFGLVDGLNFAVQYQKNGNPSGEGFTSGVTNNGRDLRONGDVGSGSTYYDY 209
DB 150 ATYRNTDFGLVDGLNFAVQYQKNGNPSGEGFTSGVTNNGRDLRONGDVGSGSTYYDY 209
QY 210 EGFGLGAISSSKRTDAQNTAAIYGNDRAEYTGGLKYDANNITYLAAQYOTYTNATRVG 269
   210 EGFGLGAISSSKRTDAQNTAAIYGNDRAEYTGGLKYDANNITYLAAQYOTYTNATRVG 269
DB 210 EGFGLGAISSSKRTDAQNTAAIYGNDRAEYTGGLKYDANNITYLAAQYOTYTNATRVG 269
QY 270 SLGMANKAQNFEAVAOYQDFGLRPSLAYLQSKGNLGRGYDDEDILKYVDGATYYFNK 329
   270 SLGMANKAQNFEAVAOYQDFGLRPSLAYLQSKGNLGRGYDDEDILKYVDGATYYFNK 329
DB 270 SLGMANKAQNFEAVAOYQDFGLRPSLAYLQSKGNLGRGYDDEDILKYVDGATYYFNK 329
QY 330 NMSTYDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367
   330 NMSTYDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367
DB 330 NMSTYDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 367
TYPE: PRT
ORGANISM: Escherichia coli
US-09-646-925-4

Query Match 59.4%; Score 218; DB 20; Length 367;
Best Local Similarity 100.0%; Pred. No. 2.1e-210;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 ATYRNTDFGLVDGLNFAYOYQGNKNGPSGEGTSGVTNNGRDLRONGDVGSGSTTYD 209
DB 150 ATYRNTDFGLVDGLNFAYOYQGNKNGPSGEGTSGVTNNGRDLRONGDVGSGSTTYD 209
QY 210 EGGIGGAISSSKRTDAQNTAAIYINGDRAETTYGKLYDANNIYLAAYOTQYNNATRVG 269
DB 210 EGGIGGAISSSKRTDAQNTAAIYINGDRAETTYGKLYDANNIYLAAYOTQYNNATRVG 269
QY 270 SLGMAKKAQNEFAVAOYQDFGLRPSLAYQSKKNLGRGYDDEDLIKYDVGATYYFNK 329
DB 270 SLGMAKKAQNEFAVAOYQDFGLRPSLAYQSKKNLGRGYDDEDLIKYDVGATYYFNK 329
QY 330 NMSTYVDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367
DB 330 NMSTYVDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367

RESULT 8
PCT-US01-08631-55900

Sequence 55900, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 55900
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (148)..(171)
OTHER INFORMATION: ECOLI/SALMONELLA-TYPE PORIN SIGNATURE domain identified by
OTHER INFORMATION: EMATRIX, accession number PR00183D, p-value=1.333e-27, raw score
OTHER INFORMATION: 9.11
NAME/KEY: DOMAIN
LOCATION: (27)..(328)
OTHER INFORMATION: General diffusion Gram-negative porins domain identified by
OTHER INFORMATION: Pfam, accession name Gram-ve_porins, E-value=3.6e-193, Pfam score
OTHER INFORMATION: of 633.8
PCT-US01-08631-55900

Query Match 42.8%; Score 157; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 6e-149;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GEGIGGAISSSKRTDAQNTAAIYINGDRAETTYGKLYDANNIYLAAYOTQYNNATRVG 270
DB 172 GEGIGGAISSSKRTDAQNTAAIYINGDRAETTYGKLYDANNIYLAAYOTQYNNATRVG 231
QY 271 LGWANKAQNFEVAOYQDFGLRPSLAYQSKKNLGRGYDDEDLIKYDVGATYYFNK 330

DB 232 LGWANKAQNFEVAOYQDFGLRPSLAYQSKKNLGRGYDDEDLIKYDVGATYYFNK 291
QY 331 MSTYVDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367
DB 292 MSTYVDYKINLLDNOFTRDAGINTDNIYALGLVYQF 328

RESULT 9
PCT-US01-08631-56227
Sequence 56227, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 56227
LENGTH: 759
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (178)..(207)
OTHER INFORMATION: KW REPLICATION REPB REPA INITIATION domain identified by
OTHER INFORMATION: EMATRIX, accession number DM00653A, p-value=7.207e-27, raw sco
OTHER INFORMATION: 20.40
NAME/KEY: DOMAIN
LOCATION: (458)..(759)
OTHER INFORMATION: General diffusion Gram-negative porins domain identified by
OTHER INFORMATION: Pfam, accession name Gram-ve_porins, E-value=3.6e-193, Pfam sc
OTHER INFORMATION: of 633.8
PCT-US01-08631-56227

Query Match 42.8%; Score 157; DB 1; Length 759;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 211 GEGIGGAISSSKRTDAQNTAAIYINGDRAETTYGKLYDANNIYLAAYOTQYNNATRVG 270
DB 603 GEGIGGAISSSKRTDAQNTAAIYINGDRAETTYGKLYDANNIYLAAYOTQYNNATRVG 662
QY 271 LGWANKAQNFEVAOYQDFGLRPSLAYQSKKNLGRGYDDEDLIKYDVGATYYFNK 330
DB 663 LGWANKAQNFEVAOYQDFGLRPSLAYQSKKNLGRGYDDEDLIKYDVGATYYFNK 722
QY 331 MSTYVDYKINLLDNOFTRDAGINTDNIYALGLVYQF 367
DB 723 MSTYVDYKINLLDNOFTRDAGINTDNIYALGLVYQF 759

RESULT 10
PCT-US01-08631-60152

Sequence 60152, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 60152

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; LENGTH: 759
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (178)..(207)
; OTHER INFORMATION: kw REPLICATION REPB REPA INITIATION domain identified by
; OTHER INFORMATION: EMATRIX, accession number DM00653a, p-value=7.207e-27, raw score
; OTHER INFORMATION: 20.40
; NAME/KEY: DOMAIN
; LOCATION: (458)..(759)
; OTHER INFORMATION: General diffusion Gram-negative porins domain identified by
; OTHER INFORMATION: Pfam, accession name Gram-ve_porins, E-value=3.6e-193, Pfam score
; OTHER INFORMATION: of 633.8
PCT-US01-08631-60152
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Query Match 42.8%; Score 157; DB 1; Length 759;
Best local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 211 GFGIGAISSSKRTDAONTAAYIGNGRATETTYGGLKYDANNITYLAQYTOTYATRVGS 270
      |||||||
Db 603 GFGIGAISSSKRTDAONTAAYIGNGRATETTYGGLKYDANNITYLAQYTOTYATRVGS 662
      |||||||
QY 271 LGMANKQNEEAVAYQYDFGLRPSLAYLQSKGNLGRGYDDEDILKYVDVGATYFNKN 330
      |||||||
Db 663 LGMANKQNEEAVAYQYDFGLRPSLAYLQSKGNLGRGYDDEDILKYVDVGATYFNKN 722
      |||||||
QY 331 MSTYVDYKINLDDNOFTRDAGINTDNIVALGLVYGF 367
      |||||||
Db 723 MSTYVDYKINLDDNOFTRDAGINTDNIVALGLVYGF 759
      |||||||
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```

RESULT 11
PCT-US01-08631-55901
; Sequence 55901, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 55901
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (186)..(209)
; OTHER INFORMATION: ECOLI/SALMONELLA-TYPE PORIN SIGNATURE domain identified by
; OTHER INFORMATION: EMATRIX, accession number PR00183D, p-value=1.333e-27, raw score
; OTHER INFORMATION: 9.11
; NAME/KEY: DOMAIN
; LOCATION: (65)..(312)
; OTHER INFORMATION: General diffusion Gram-negative porins domain identified by
; OTHER INFORMATION: Pfam, accession name Gram-ve_porins, E-value=2.2e-145, Pfam score
; OTHER INFORMATION: of 477.5
PCT-US01-08631-35901
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Query Match 34.6%; Score 127; DB 1; Length 393;
Best local Similarity 100.0%; Pred. No. 1.2e-118;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 21 AAEVYNKDGKRLDYGKVDGLHYFSDNKKDVGDTYMRIGFGKGTQVTDLTGYGQWEYQ 80
      |||||||
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Db 59 AAEVYNKDGKRLDYGKVDGLHYFSDNKKDVGDTYMRIGFGKGTQVTDLTGYGQWEYQ 118
      |||||||
QY 81 IQGNSAENENNSWTRVAFAGLKFQDVGSFQYGRNRYGVYDVTSTVDLPERGGGTYSND 140
      |||||||
Db 119 IQGNSAENENNSWTRVAFAGLKFQDVGSFQYGRNRYGVYDVTSTVDLPERGGGTYSND 178
      |||||||
QY 141 FMOORGN 147
      |||||||
Db 179 FMOORGN 185
      |||||||
```

RESULT 12
PCT-US01-08631-56224
; Sequence 56224, Application PC/TUS0108631
; GENERAL INFORMATION:

```

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56224
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (58)..(79)
; OTHER INFORMATION: General diffusion Gram-negative porins domain identified by
; OTHER INFORMATION: EMATRIX, accession number BL00576a, p-value=2.96
; OTHER INFORMATION: 21, raw score of 15.07
; NAME/KEY: DOMAIN
; LOCATION: (27)..(161)
; OTHER INFORMATION: General diffusion Gram-negative porins domain identified by
; OTHER INFORMATION: Pfam, accession name Gram-ve_porins, E-value=1.2e-83, Pfam sco
; OTHER INFORMATION: misc-feature
; LOCATION: (1)..(501)
; OTHER INFORMATION: xaa = x or * as defined in Table 2
PCT-US01-08631-56224
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Query Match 21.5%; Score 79; DB 1; Length 501;
Best local Similarity 100.0%; Pred. No. 3.8e-70;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 21 AAEVYNKDGKRLDYGKVDGLHYFSDNKKDVGDTYMRIGFGKGTQVTDLTGYGQWEYQ 80
      |||||||
Db 21 AAEVYNKDGKRLDYGKVDGLHYFSDNKKDVGDTYMRIGFGKGTQVTDLTGYGQWEYQ 80
      |||||||
QY 81 IQGNSAENENNSWTRVAF 99
      |||||||
Db 81 IQGNSAENENNSWTRVAF 99
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Search completed: August 1, 2002, 10:54:55
Job time: 218 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 1, 2002, 10:51:37 ; Search time 26.07 Seconds
(without alignments)
2114.834 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 367
Sequence: 1 MKSKVLALLIPALLAGAAH.....TRDAGINTDNIVAGLVYQF 367

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 461083 seqs, 150228150 residues

Word size : 50

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending_Patents_AA_New:*
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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description

No matches found				

Search completed: August 1, 2002, 10:55:27
Job time: 230 sec

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Db 210 egfgigaissskrtidaqntaaylgnqdraetyglkydanniylaaytqctynatrv 269
QY 270 SLGWANKAQNFEAVAOYQDFGLRPSLAYQSGKNLGRGYDDEDILKYVDGATYYFNK 329
Db 270 slgwankagnfeavaqygfifglrpslaylqskgknlgryddedllkyvdgatltyfnk 329
QY 330 NMSTYVDYKINLLDDNOFTRDAGINTDNIVALGLVYQF 367
Db 330 nmstlyvdykinnliddnqftrdagintdnivalglvyqf 367

RESULT 2
AA34058
ID AAY34058 standard; protein; 367 AA.
XX
AC AAY34058;
XX
DT 23-NOV-1999 (first entry)
XX
DE E. coli outer membrane protein c precursor.
XX
KM Ulcerative colitis; histone: H1-like antigen; porin antigen;
KM Bacteroides antigen; IB: PANCA; inflammatory bowel disease;
KM diagnosis; perinuclear anti-neutrophil cytoplasmic antibody;
KM outer membrane protein c precursor.
XX
OS Escherichia coli.
XX
PN W09945955-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05492.
XX
PR 12-MAR-1998; 98US-0041889.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Braun J, Cohavy O;
XX
DR WPI; 1999-551215/46.
XX
PT Use of histone H1, porin or Bacteroides antigens as targets for the
PT diagnosis, prevention and treatment of ulcerative colitis -
XX
PS Claim 8; Fig 11; 134pp; English.
XX
CC The invention provides a method for the diagnosis, prevention and
CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a
CC porin antigen or a Bacteroides antigen as a target antigen. The novel
CC method of diagnosing UC in a subject suspected of having inflammatory
CC bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
CC (2) contacting the sample with a histone H1-like antigen, or perinuclear
CC anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form a
CC complex of the histone H1-like antigen, or the PANCA-reactive fragment,
CC and antibody to the histone H1-like antigen; and (3) detecting the
CC presence or absence of the complex; where the presence of the complex
CC indicates that the subject has UC. The PANCA-reactive histone H1-like
CC antigen, porin antigen and Bacteroides antigen are useful in the
CC diagnosis, prevention and treatment of UC. The methods can also be used
CC for identifying agents useful for treating UC. The present sequence
CC represents a E. coli outer membrane protein c precursor.
XX
SQ Sequence 367 AA;

Query Match 59.4%; Score 218; DB 20; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.1e-203;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 ATYRNDFPGLVGLNFAVYOGKNGNPSGEGFTSGVTNNGRDLRONGGVGSGSTYYDY 209
Db 150 atyrndfpglvglnfavvygkngnpsgeftsgvtmngdrlrngdvgsgstlydy 209

QY 210 EGFIGIGAISSSKRTDAQNTAAVYIGNDRAETTYGGLKYDANNIYLAAYTQCTYNATRV 269
Db 210 egfgigaissskrtidaqntaaylgnqdraetyglkydanniylaaytqctynatrv 269
QY 270 SLGWANKAQNFEAVAOYQDFGLRPSLAYQSGKNLGRGYDDEDILKYVDGATYYFNK 329
Db 270 slgwankagnfeavaqygfifglrpslaylqskgknlgryddedllkyvdgatltyfnk 329
QY 330 NMSTYVDYKINLLDDNOFTRDAGINTDNIVALGLVYQF 367
Db 330 nmstlyvdykinnliddnqftrdagintdnivalglvyqf 367

RESULT 3
AAY57356
ID AAY57356 standard; protein; 367 AA.
XX
AC AAY57356;
XX
DT 13-JUN-2000 (first entry)
XX
DE E. coli outer membrane protein c precursor.
XX
KM Ulcerative colitis; inflammatory bowel disease; porin antigen; Mab;
KM PANCA; perinuclear anti-neutrophil cytoplasmic antibody;
KM histone H1; outer membrane protein c precursor.
XX
OS Escherichia coli.
XX
PN US6033864-A.
XX
PD 07-MAR-2000.
XX
PF 12-MAR-1998; 98US-0041889.
XX
PR 12-APR-1996; 96US-0057846.
XX
PR 11-APR-1997; 97US-0837058.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cohavy O, Braun J;
XX
DR WPI; 2000-255695/22.
XX
PT Diagnosing ulcerative colitis or susceptibility, by detecting complex
PT formation between microbial porin antigen and perinuclear
PT anti-neutrophil cytoplasmic autoantibodies -
XX
PS Claim 1; Fig 10; 49pp; English.
XX
CC The invention provides a method for diagnosing ulcerative colitis in a
CC subject suspected of having inflammatory bowel disease. The method
CC comprises reacting a patient sample with a porin antigen that is
CC immunologically reactive with PANCA (perinuclear anti-neutrophil
CC cytoplasmic antibodies) and detecting formation of a Ag-PANCA complex
CC as indicative of ulcerative colitis. The method is used to diagnose
CC ulcerative colitis or susceptibility to it. The present sequence
CC represents a E. coli outer membrane protein c precursor.
XX
SQ Sequence 367 AA;

Query Match 59.4%; Score 218; DB 21; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.1e-203;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 ATYRNDFPGLVGLNFAVYOGKNGNPSGEGFTSGVTNNGRDLRONGGVGSGSTYYDY 209
Db 150 atyrndfpglvglnfavvygkngnpsgeftsgvtmngdrlrngdvgsgstlydy 209
QY 210 EGFIGIGAISSSKRTDAQNTAAVYIGNDRAETTYGGLKYDANNIYLAAYTQCTYNATRV 269
Db 210 egfgigaissskrtidaqntaaylgnqdraetyglkydanniylaaytqctynatrv 269

Db 210 egfgiagaissskrtidagntaaylgnngdraetcytgglkydanniylaagylqfynatrvy 269
QY 270 SLGMANKAQNFEAVAOYQDFGRLPSLAYLOSCKNLGRCYDDEDILKYDVGNATYFNK 329
Db 270 slgwnakagnteavayqgfdfglrpslaylqskgknlgrgyddedilkydvgaetyfnk 329
QY 330 NMSTYVDYKINLDDNQFTRDAGINTDNIVALGLVYQF 367
Db 330 mstlyvdyklnliddngftrdagintdnivalglvyqf 367

RESULT 4
ABG25541
ID ABG25541 standard; Protein: 328 AA.
XX
AC ABG25541;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #25532.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
PI
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS89728.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
PS Claim 20; SEQ ID No 55900; 103pp; English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 328 AA;

Query Match 42.8%; Score 157; DB 22; Length 328;
Best Local Similarity 100.0%; Pred. No. 2.4e-144;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 211 GFGIGGAISSSKRTDAQNFAAYIGNGDRAETTYGGLKRYDANNIYLAAYOTYNAFRVGS 270
Db 172 gfgiggaisskrtidagntaaylgnngdraetcytgglkydanniylaagylqfynatrvy 231
QY 271 LGMANKAQNFEAVAOYQDFGRLPSLAYLOSCKNLGRCYDDEDILKYDVGNATYFNKN 330
Db 232 lqwnakagnteavayqgfdfglrpslaylqskgknlgrgyddedilkydvgaetyfnkn 291
QY 331 MSTYVDYKINLDDNQFTRDAGINTDNIVALGLVYQF 367
Db 292 mstlyvdyklnliddngftrdagintdnivalglvyqf 328

RESULT 5
ABG25868
ID ABG25868 standard; Protein: 759 AA.
XX
AC ABG25868;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #25859.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
PI
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS90055.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
PS Claim 20; SEQ ID No 56227; 103pp; English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human

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OM protein - protein search, using sw model

Run on: August 1, 2002, 10:48:47 ; Search time 13.19 Seconds
(without alignments)
679.620 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 367
Sequence: 1 MKSKVLLALIRALLAAGAAH.....TRDAGINTDNIVALGLVYGF 367

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Gapop 60.0 , Gapext 60.0

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Word size : 50

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	218	59.4	367	3	US-09-041-889-30

ALIGNMENTS

RESULT 1
US-09-041-889-30
; Sequence 30, Application US/09041889
; Patent No. 6033864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,058
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-041-889-30

Query Match 59.4%; Score 218; DB 3; Length 367;
Best Local Similarity 100.0%; Pred. No. 1.4e-196;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	150	ATYRNTDFGLVGLNFAVQYOGKNGNPSGEGFTSGVTNNGRDALRONGDVGSGSITYDY	209
DB	150	ATYRNTDFGLVGLNFAVQYOGKNGNPSGEGFTSGVTNNGRDALRONGDVGSGSITYDY	209
QY	210	EGFGIGAISSSKRTDAQNTAAIYIGNCDRAETTYGGLKYDANNITYLAAQTYQYNAFRVG	269
DB	210	EGFGIGAISSSKRTDAQNTAAIYIGNCDRAETTYGGLKYDANNITYLAAQTYQYNAFRVG	269
QY	270	SLGMANKAQNFEVAVOQFPGFLRPSLAYLQSKGNLGRGVDDDDILKYDVGATYYFNK	329
DB	270	SLGMANKAQNFEVAVOQFPGFLRPSLAYLQSKGNLGRGVDDDDILKYDVGATYYFNK	329
QY	330	NMSTYYDYKINLLDDNQFTRDAGINTDNIVALGLVYGF	367
DB	330	NMSTYYDYKINLLDDNQFTRDAGINTDNIVALGLVYGF	367

Search completed: August 1, 2002, 10:52:30
Job time: 223 sec

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OM protein - protein search, using sw model

Run on: August 1, 2002, 10:50:42 ; Search time 21.04 Seconds
(without alignments)
1676.083 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 367
Sequence: 1 MRSKYLALLIPALLAAGAAH.....TRDAGINTDNIVALGLVYQF 367

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 segs, 96089334 residues

Word size : 50

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : PIR-71:*
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2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	218	59.4	367	1 MMEPC	outer membrane por
2	98	26.7	367	2 H91016	outer membrane pro
3	98	26.7	367	2 B85861	outer membrane pro

ALIGNMENTS

RESULT 1
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outer membrane porin ompC precursor - Escherichia coli
C/Species: Escherichia coli
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C/Accession: A20867, A18885, B25029, E64991
R/Mizuno, T.; Chou, M.Y.; Inouye, M.
J. Biol. Chem. 258, 6932-6940, 1983
A/Title: A comparative study on the genes for three porins of the Escherichia coli outer
A/Reference number: A20867, MUID:83213433
A/Accession: A20867
A/Molecule type: DNA
A/Residues: 1-367 <MI2>
A/Cross-references: GB:K00541; GB:M10314; GB:M14188; NID:9147007; PIDN:AAA24243.1; PID:9
R:Mizuno, T.; Chou, M.Y.; Inouye, M.
FEBS Lett. 151, 159-164, 1983
A/Title: DNA sequence of the promoter region of the ompC gene and the amino acid sequenc
A/Accession: A18885
A/Reference number: A18885, MUID:83132326
A/Molecule type: DNA
A/Residues: 1-40 <MI2>

R:Nogami, T.; Mizuno, T.; Mizushima, S.
J. Bacteriol. 164, 797-801, 1985
A/Title: Construction of a series of ompC-ompC chimeric genes by in vivo homologous r
A/Reference number: A91809; MUID:06033642
A/Accession: B25029
A/Molecule type: DNA
A/Residues: 32-57 <NOG>
R:Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617
A/Accession: E64991
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-367 <PLAT>
A/Cross-references: GB:AE000310; GB:U00096; NID:g2367131; PIDN:AACT5275.1; PID:g17885
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A:Gene: ompC
A:Map position: 47 min
C/Function:
A/Description: one of the E. coli major outer membrane proteins that form passive dif
C/Superfamily: outer membrane protein phoE
C/Keywords: membrane protein; porin; trimer
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F:22-367/Product: outer membrane porin ompC #status predicted <MAT>

Query Match 59.4%; Score 218; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 7.7e-211;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	210	EGFGTIGAISSSKRTDQNTAAATGNGDRRAETTYGKLYAANNITLYLAOYTOTYNNATRVG	269
DB	210	EGFGTIGAISSSKRTDQNTAAATGNGDRRAETTYGKLYAANNITLYLAOYTOTYNNATRVG	269
QY	270	SLGWANKAQNFEAVAYQYQFDFGLRPSLAYLQSKGNLGRGYDEDLKYVDVGAATYYFNK	329
DB	270	SLGWANKAQNFEAVAYQYQFDFGLRPSLAYLQSKGNLGRGYDEDLKYVDVGAATYYFNK	329
QY	330	NMSYVDYKINLDDNOFTRDAGINTDNIVALGLVYQF	367
DB	330	NMSYVDYKINLDDNOFTRDAGINTDNIVALGLVYQF	367

RESULT 2
H91016
outer membrane protein C ompC ECS3104 [imported] - Escherichia coli (strain O157:H7,
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C/Accession: H91016
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kunita, S.; Shida, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: H91016
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-367 <HAY>
A/Cross-references: GB:BA000007; PIDN:BA836527.1; PID:g13362573; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A:Gene: ECS3104
C/Superfamily: outer membrane protein phoE
Query Match 26.7%; Score 98; DB 2; Length 367;

Best Local Similarity 100.0%; Pred. No. 3.4e-90;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 50 VDDGQTYMRLEFGKQVTDQLNGYGOMEXIOGNSAENENNSWTRVAFAGLKFQDVGSPF 109

OY 110 DYGRNYGVVYDVTSWTDVLPFEGGDTYGSDFNQQRGN 147
|||||
Db 110 DYGRNYGVVYDVTSWTDVLPFEGGDTYGSDFNQQRGN 147

RESULT 3

B85861

outer membrane protein 1b (Ibc) [imported] - Escherichia coli (strain O157:H7, substrain C; Date: 16-Feb-2001 #sequence, revision 16-Feb-2001 #text_change 14-Sep-2001

C; Accession: B85861

R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Iller, L.; Grothbeck, E.J.; Davis, N.W.; Llin, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Accession: B85861

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-367 <STO>

A; Cross-references: GB:AE005174; NID:g12516550; PIDN:AG57350.1; GSPDB:GN00145; UWCP:234

A; Experimental source: strain O157:H7, substrain EDL933

C; Genetics:

A; Gene: ompC

C; Superfamily: outer membrane protein phoE

Query Match 26.7%; Score 98; DB 2; Length 367;

Best Local Similarity 100.0%; Pred. No. 3.4e-90;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 VDDGQTYMRLEFGKQVTDQLNGYGOMEXIOGNSAENENNSWTRVAFAGLKFQDVGSPF 109
|||||

Db 50 VDDGQTYMRLEFGKQVTDQLNGYGOMEXIOGNSAENENNSWTRVAFAGLKFQDVGSPF 109

OY 110 DYGRNYGVVYDVTSWTDVLPFEGGDTYGSDFNQQRGN 147
|||||

Db 110 DYGRNYGVVYDVTSWTDVLPFEGGDTYGSDFNQQRGN 147

Search completed: August 1, 2002, 10:52:58
Job time: 136 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 1, 2002, 10:52:32 ; Search time 13.48 seconds

(without alignments)
1054.160 Million cell updates/sec

Title: US-09-575-061-1

Perfect score: 367
Sequence: 1 MMSKVLALLIPALLAAGAAH.....TRDAGINTNDIVALLGLVYQF 367

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 50

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	218	59.4	367 1 OMPC_ECOLI	P06996 escherichia

ALIGNMENTS

RESULT 1
OMPC_ECOLI STANDARD; PRT; 367 AA.
AC P06996;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein C precursor (Porin ompC) (Outer membrane protein 1B).
DE OMPC OR MEDA OR PAR OR B2215.
GN Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83213433; PubMed=6304064;
RA Mizuno T., Chou M.-Y., Inouye M.;
RT "A comparative study on the genes for three porins of the Escherichia coli outer membrane. DNA sequence of the osmoregulated ompC gene."; J. Biol. Chem. 258:6932-6940(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y., Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 218-367 FROM N.A.
RC STRAIN=K12 / BHB2600;
RA Richerich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K., Church G.M.;
RT Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-22 FROM N.A., AND SEQUENCE OF 22-40.
RX MEDLINE=83132326; PubMed=6297988;
RA Mizuno T., Chou M.-Y., Inouye M.;
RT "DNA sequence of the promoter region of the ompC gene and the amino acid sequence of the signal peptide of pro-ompC protein of Escherichia coli."; FEBS Lett. 151:159-164(1983).
RN [6]
RP SEQUENCE OF 33-57 FROM N.A.
RX MEDLINE=86033642; PubMed=2997131;
RA Nogami T., Mizuno T., Mizushima S.;
RT "Construction of a series of ompC-ompC chimeric genes by in vivo homologous recombination in Escherichia coli and characterization of the translational products."; J. Bacteriol. 164:797-801(1985).
RN [7]
RP SEQUENCE OF 22-30.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
RN [8]
RP SEQUENCE OF 22-26.
RC STRAIN=K12 / W3110;
RX MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M., Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
RT "Extraction of membrane proteins by differential solubilization for separation using two-dimensional gel electrophoresis."; Electrophoresis 19:837-844(1998).
RN [9]
RP FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein, outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHO FAMILY OF PORINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL: K00541; AAA24243.1;
CC EMBL: AE000310; AAC75275.1;
CC EMBL: D90850; BAA15998.1; -.

DR EMBL: U00008; AA16412.1; -.
DR PIR: A20867; MMEPC.
DR PIR: B25029; B25029.
DR PIR: A18885; A18885.
DR HSSP: P09878; 1IIV.
DR ECODBASE: A035.5; 6TH EDITION.
DR Ecogene; Egi0670; ompC.
DR InterPro; IPR001702; Gram_neg_porin.
DR Pfam; PF00267; Gram-ve_porins; 1.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal;
KW Complete proteome.
FT SIGNAL 1 21
FT CHAIN 22 367 OUTER MEMBRANE PROTEIN C.
SQ SEQUENCE 367 AA; 40368 MW; 6A49370CC8A1A225 CRC64;

Query Match 59.4%; Score 218; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 4.5e-210;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 ATYRNTDFGLVDGLNFAVOYOGKNGNPSEGEFTSGVTNNGRDALRONGDVGGSITYDY 209
DB 150 ATYRNTDFGLVDGLNFAVOYOGKNGNPSEGEFTSGVTNNGRDALRONGDVGGSITYDY 209
OY 210 EGRGIGGATISSKRTDAONTAAITGNGDRAETTYGGLKYDANNIYLAQYTYTNATRVG 269
DB 210 EGRGIGGATISSKRTDAONTAAITGNGDRAETTYGGLKYDANNIYLAQYTYTNATRVG 269
OY 270 SIGWANKAONFEAVAYOYQDFEGLRPSLAYIQSKKNLGRGYDDEDIILKYVDGATYYFNK 329
DB 270 SIGWANKAONFEAVAYOYQDFEGLRPSLAYIQSKKNLGRGYDDEDIILKYVDGATYYFNK 329
OY 330 NMSTYVDYKINILDDNOFTPDAGINTDNIYALGLVYQF 367
DB 330 NMSTYVDYKINILDDNOFTPDAGINTDNIYALGLVYQF 367

Search completed: August 1, 2002, 10:56:22
Job time: 230 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 1, 2002, 10:52:12 ; Search time 28.25 Seconds
(without alignments)
2247.403 Million cell updates/sec

Title: US-09-575-061-1
Perfect score: 367
Sequence: 1 MKSKYALALIPALAAAGAH.....TRDAGINTDNIVALGLVYGF 367

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 50

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

SPPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	30.0	364	09K597	09K597 escherichia
2	98	26.7	366	09RH85	09rh85 escherichia

ALIGNMENTS

RESULT 1
09K597
ID 09K597 PRELIMINARY; PRT; 364 AA.
AC 09K597;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PORIN C PRECURSOR.
GN OMPC.

OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Low A.S., Mackenzie F.M., Gould I.M., Booth I.R.;
RT "Parallel evolution of multi-resistant bacteria in a patient with recurrent septicaemia: unique data that support the presence of separate protected environments."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE (BY SIMILARITY).
DR EMBL: AJ295721; CAC01403-1; -
DR HSSP: P09878; IITV.
DR InterPro: IPR001702; Gram_neg_porin.
DR InterPro: IPR000504; RM.
DR Pfam: PF00267; Gram-ve_porins.1.
DR PRINTS: PR00182; ECOLNEIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN.1.
DR PROSITE: PS00030; RM_RNP_1; UNKNOWN_1.
KW Outer membrane; Porin; Signal; Transmembrane.
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 364 AA; 40312 MW; 9B583F2C11344E31 CRC64;

Query Match 30.0%; Score 110; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-100;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 236 GDRAEYTGGLKYDANNIYLAQYOTYNATRVGSLGANKAQNFEAVAOYDFGLRPS 295
DB 233 GDRAEYTGGLKYDANNIYLAQYOTYNATRVGSLGANKAQNFEAVAOYDFGLRPS 292
OY 296 LAYLSKSKNLGRGYDEDIKYVDGATYFFNKNMSTYVDYKINLDDN 345
DB 293 LAYLSKSKNLGRGYDEDIKYVDGATYFFNKNMSTYVDYKINLDDN 342

RESULT 2
09RH85
ID 09RH85 PRELIMINARY; PRT; 366 AA.
AC 09RH85;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN OMPC.
GN OMPC.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=O157:H7;
RA Yu S.L., Syu W.J.;
RT "Altered outer membrane protein Ompc in hemorrhagic Escherichia coli O157:H7."
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE (BY SIMILARITY).
DR EMBL: AF057355; AF21761.1; -
DR HSSP: P09878; IITV.
DR InterPro: IPR001702; Gram_neg_porin.
DR Pfam: PF00267; Gram-ve_porins.1.
DR PRINTS: PR00182; ECOLNEIPORIN.
DR PROSITE: PS00576; GRAM_NEG_PORIN.1.
KW Outer membrane; Porin; Signal; Transmembrane.
SQ SEQUENCE 366 AA; 40499 MW; 6A4EAD1652565C00 CRC64;

Query Match 26.78; Score 98; DB 2; Length 366;
 Best Local Similarity 100.0%; Pred. No. 1.4e-88;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 VDDQDTYMRIGFKGETQVTDQLTGYGOMEYOIOGNSAENENNSWTRVAFAGLKFQDYGSF 109
 |||
 Db 50 VDDQDTYMRIGFKGETQVTDQLTGYGOMEYOIOGNSAENENNSWTRVAFAGLKFQDYGSF 109

QY 110 DYGRNYGVVYDVTSMEDVLPFPGSDTYGSDNFMQQRGN 147
 |||
 Db 110 DYGRNYGVVYDVTSMEDVLPFPGSDTYGSDNFMQQRGN 147

Search completed: August 1, 2002, 10:56:02
 job time: 230 sec